

Figure 1

85P1B3 SSH sequence and GenBank homology to OIP5

GATCAGAGGACACATGGGACTCTGCATCTTAATTCCTAAATTTACAGTCAAAGACATTTTCAG
AGATAAGTATTATGAATTCAATAAGAATCTAAAGTAAGTTCTTAAGGCAAATAGCTATAAAA
GAGAAGAATCCTTAGTCTCTCATCTTCTAAAAACAGCTTCACAAATAATTTGGAAAATCAGCC
TAAAGGTAAATAGAACTGCATTTCCCTCCATTCTTGAAGCCAATCTTTTCAAGAAATGAC
TAAGCAGCACCTGTTGTTGAAGACAGCAATAAAGCCTGAACCTGACACTCAAGCTTTGGTACA
GGATC

gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein... 632 e-179
gb|AF158642.1|AF158642 Homo sapiens metalloproteinase-disin... 42 0.12
gb|AC005075.2|AC005075 Homo sapiens clone RG219E16, complet... 42 0.12
emb|AL096773.6|HS1000E10 Human DNA sequence from clone 1000... 40 0.48

>gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein OIP5 mRNA, partial cds
Length = 1197

Score = 632 bits (319), Expect = e-179
Identities = 319/319 (100%)
Strand = Plus / Minus

Query: 1 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacat ttt 60
|||||
Sbjct: 1013 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacat ttt 954

Query: 61 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatagcta 120
|||||
Sbjct: 953 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatagcta 894

Query: 121 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgga 180
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Sbjct: 893 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgga 834

Query: 181 aatcagcctaaaggtaaatagaaactgcatttccctccattcttgaagccaatctttt 240
|||||
Sbjct: 833 aatcagcctaaaggtaaatagaaactgcatttccctccattcttgaagccaatctttt 774

Query: 241 caagaaatgactaagcagcacctgttggtgaagacagcaataaagcctgaacctgacact 300
|||||
Sbjct: 773 caagaaatgactaagcagcacctgttggtgaagacagcaataaagcctgaacctgacact 714

Query: 301 caagctttggtacaggatc 319
|||||
Sbjct: 713 caagctttggtacaggatc 695

403630 "caagctttggtacaggatc"

5'	GGC	TGC	GGG	AAG	ATG	GCG	GCT	CAG	CCG	CTG	CGG	CAT	CGC	TCA	CGT	TGT	GCA	ACG	54
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			63			72			81			90			99			108	
	CCG	CCC	CGG	GGG	GAC	TTT	TGT	GGT	GGC	ACT	GAG	AGG	GCG	ATT	GAC	CAA	GCT	TCT	
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	P	P	R	G	D	F	C	G	G	T	E	R	A	I	D	Q	A	S	
			117			126			135			144			153			162	
	TTT	ACG	ACC	TCC	ATG	GAG	TGG	GAT	ACG	CAG	GTG	GTG	AAG	GGG	TCC	TCG	CCG	CTC	
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	F	T	T	S	M	E	W	D	T	Q	V	V	K	G	S	S	P	L	
			171			180			189			198			207			216	
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	G	P	A	G	L	G	A	E	E	P	A	A	G	P	Q	L	P	S	
			225			234			243			252			261			270	
	TGG	CTG	CAG	CCT	GAG	AGG	TGC	GCT	GTG	TTC	CAG	TGC	GCA	CAG	TGT	CAC	GCA	GTG	
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	W	L	Q	P	E	R	C	A	V	F	Q	C	A	Q	C	H	A	V	
			279			288			297			306			315			324	
	CTC	GCC	GAC	TCG	GTG	CAC	CTC	GCC	TGG	GAC	CTG	TCG	CGG	TCC	CTC	GGG	GCC	GTG	
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	L	A	D	S	V	H	L	A	W	D	L	S	R	S	L	G	A	V	
			333			342			351			360			369			378	
	GTC	TTC	TCC	AGA	GTT	ACA	AAT	AAC	GTC	GTT	TTG	GAA	GCG	CCC	TTC	CTA	GTT	GGC	
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	V	F	S	R	V	T	N	N	V	V	L	E	A	P	F	L	V	G	
			387			396			405			414			423			432	
	ATT	GAA	GGT	TCA	CTC	AAA	GGC	AGT	ACT	TAC	AAC	CTT	TTA	TTC	TGT	GGT	TCT	TGT	
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	I	E	G	S	L	K	G	S	T	Y	N	L	L	F	C	G	S	C	
			441			450			459			468			477			486	
	GGG	ATT	CCC	GTT	GGT	TTC	CAT	CTG	TAT	TCT	ACC	CAT	GCT	GCC	CTG	GCT	GCC	TTG	
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	G	I	P	V	G	F	H	L	Y	S	T	H	A	A	L	A	A	L	
			495			504			513			522			531			540	
	AGA	GGT	CAC	TTC	TGC	CTT	TCC	AGT											

657				666				675				684				693				702	
CTA	ATG	AAG	ATT	CTG	AGT	GAA	GTG	ACT	CCT	GAC	CAG	TCC	AAG	CCA	GAA	AAC	TGA				
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L	M	K	I	L	S	E	V	T	P	D	Q	S	K	P	E	N	*				
711				720				729				738				747				756	
TCC	TGT	ACC	AAA	GCT	TGA	GTG	TCA	GGT	TCA	GGC	TTT	ATT	GCT	GTC	TTC	AAC	AAC				
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765				774				783				792				801				810	
AGG	TGC	TGC	TTA	GTC	ATT	TCT	TGA	AAA	AGA	TTG	GCT	TCA	AGA	ATG	GAG	GGG	AAA				
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819				828				837				846				855				864	
TGC	AGT	TTC	TAT	TTA	CCT	TTA	GGC	TGA	TTT	TCC	AAA	TTA	TTT	GTG	AAG	CTG	TTT				
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873				882				891				900				909				918	
TTA	GAA	GAT	GAG	AGA	CTA	AGG	ATT	CTT	CTC	TTT	TAT	AGC	TAT	TTG	CCT	TAA	GAA				
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927				936				945				954				963				972	
CTT	ACT	TTA	GAT	TCT	TAT	TGA	ATT	CAT	AAT	ACT	TAT	CTC	TGA	AAA	TGT	CTT	TGA				
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981				990				999				1008				1017				1026	
CTG	TAA	ATT	TAG	GAA	TTA	AGA	TGC	AGA	GTC	CCA	TGT	GTC	CTC	TGA	TCT	AAA	GTT				
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1035				1044				1053				1062				1071				1080	
GCA	TGG	TTG	GTC	TGA	AAA	TAG	AGT	TGG	GCT	TAA	TGT	TGA	CTT	CTA	TTA	CTC	CTG				
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1089				1098				1107				1116				1125				1134	
CAT	GGA	GCA	GTT	GTT	ATG	AAT	ACT	AAT	ACA	TCA	CTT	TTT	AAC	TTC	TGT	AAA	ATA				
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1143				1152				1161				1170				1179				1188	
CAG	ATC	ATA	ATA	TTC	TAT	AGG	TAA	TGT	TTA	ATA	AAT	TGC	CTG	AAT	AAT	AAA	AAA				
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1197				1206				1215				1224				1233				1242	
AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA			
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1251				1260																	
AAA	AAA	AAA	AAA	AAA	AAA	AA	3'														

85P1B3/OIP5 protein sequence.

1 MAAQPLRHRS RCATPPRGDF CGGTERAIDQ ASFTTSMEDW TQVVKGS SPL GPAGLGAEEP
61 AAGPQLPSWL QPERCAVFQC AQCHAVLADS VHLLAWDLRS LGAVVFSRVT NNVVLEAPFL
121 VGIEGSLKGS TYNLLFCGSC GIPVGPHLYS THAALAALRG HFCLSSDKMV CYLLKTKAIV
181 NASEMDIQNV PLSEKIAELK EKIVLTHNRL KSLMKILSEV TPDQSKPEN*

Figure 4

Alignment of 85P1B3 with OIP5.

>gi|2815610|gb|AAC39561.1|(AF025441) Opa-interacting protein OIP5 [Homo sapiens]
Length = 231

Score = 462 bits (1189), Expect = e-130
Identities = 229/229 (100%), Positives = 229/229 (100%)

```
85P1B3: 1  MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEPP 60
      MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEPP
OIP5: 3  MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEPP 62

85P1B3: 61  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL 120
      AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL
OIP5: 63  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL 122

85P1B3:121  VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 180
      VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV
OIP5: 123  VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 182

85P1B3:181  NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 229
      NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN
OIP5: 183  NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 231
```

103660 3044600

Figure 5: 85P1B3 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

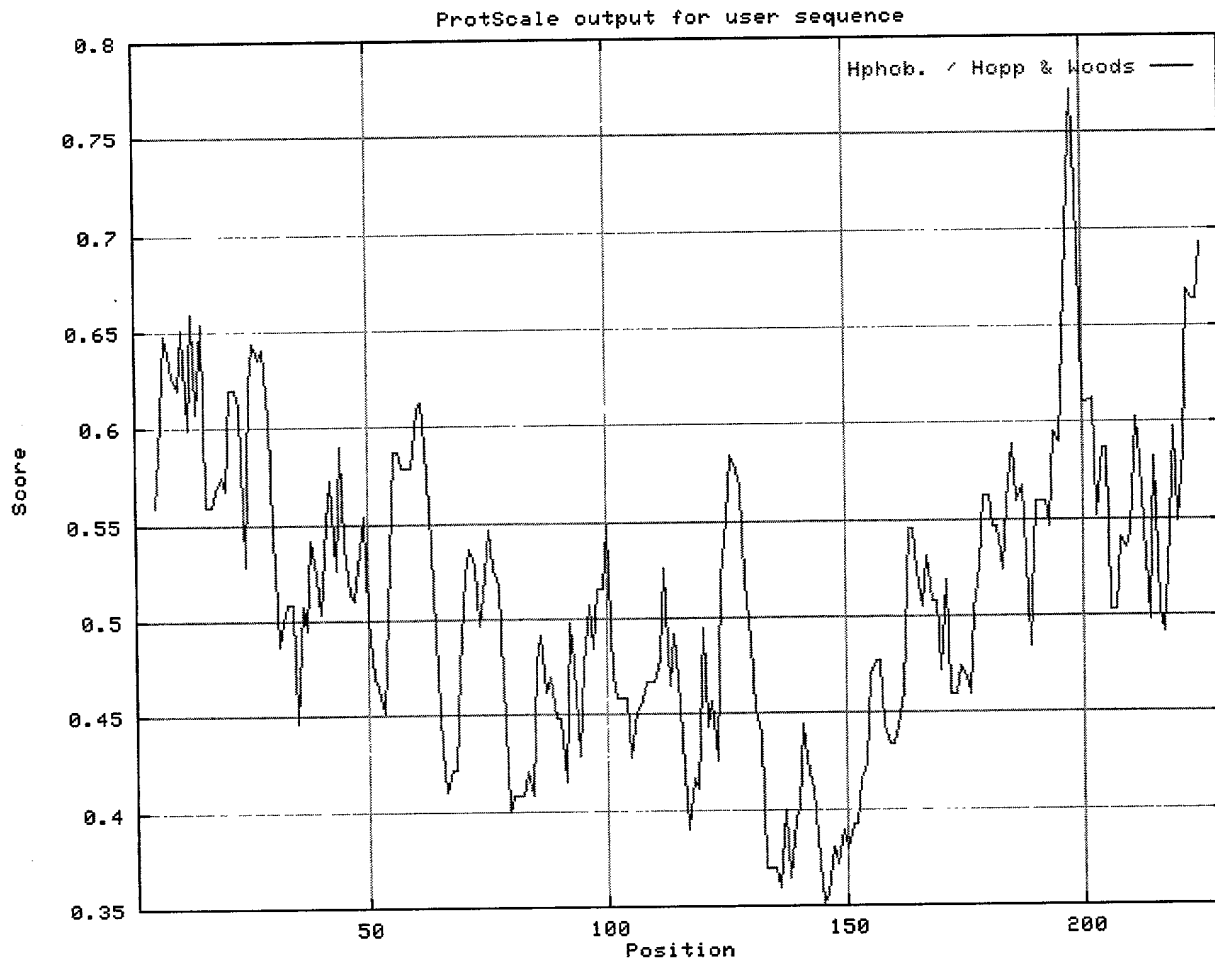


Figure 6: 85P1B3 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

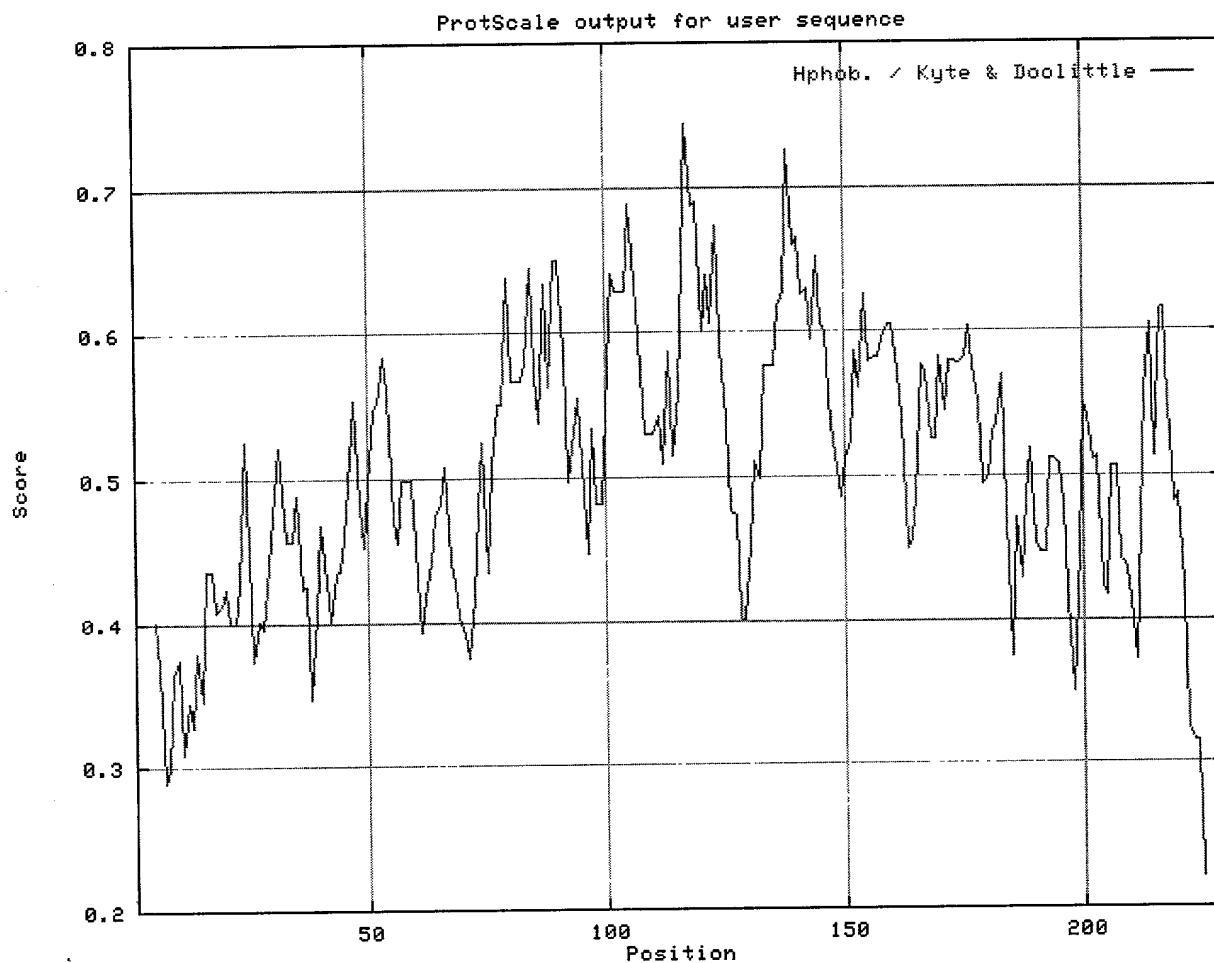


Figure 7: 85P1B3 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

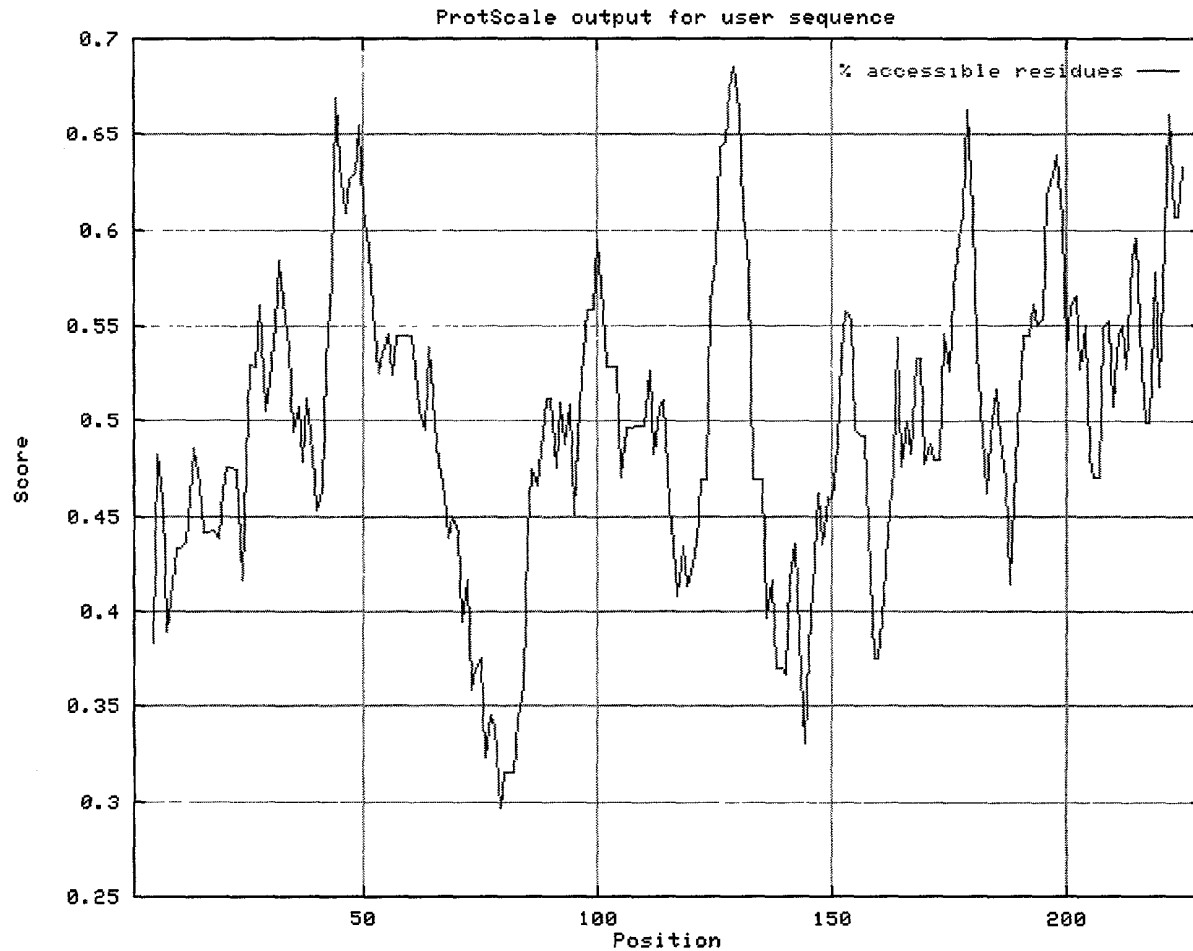


Figure 8: 85P1B3 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

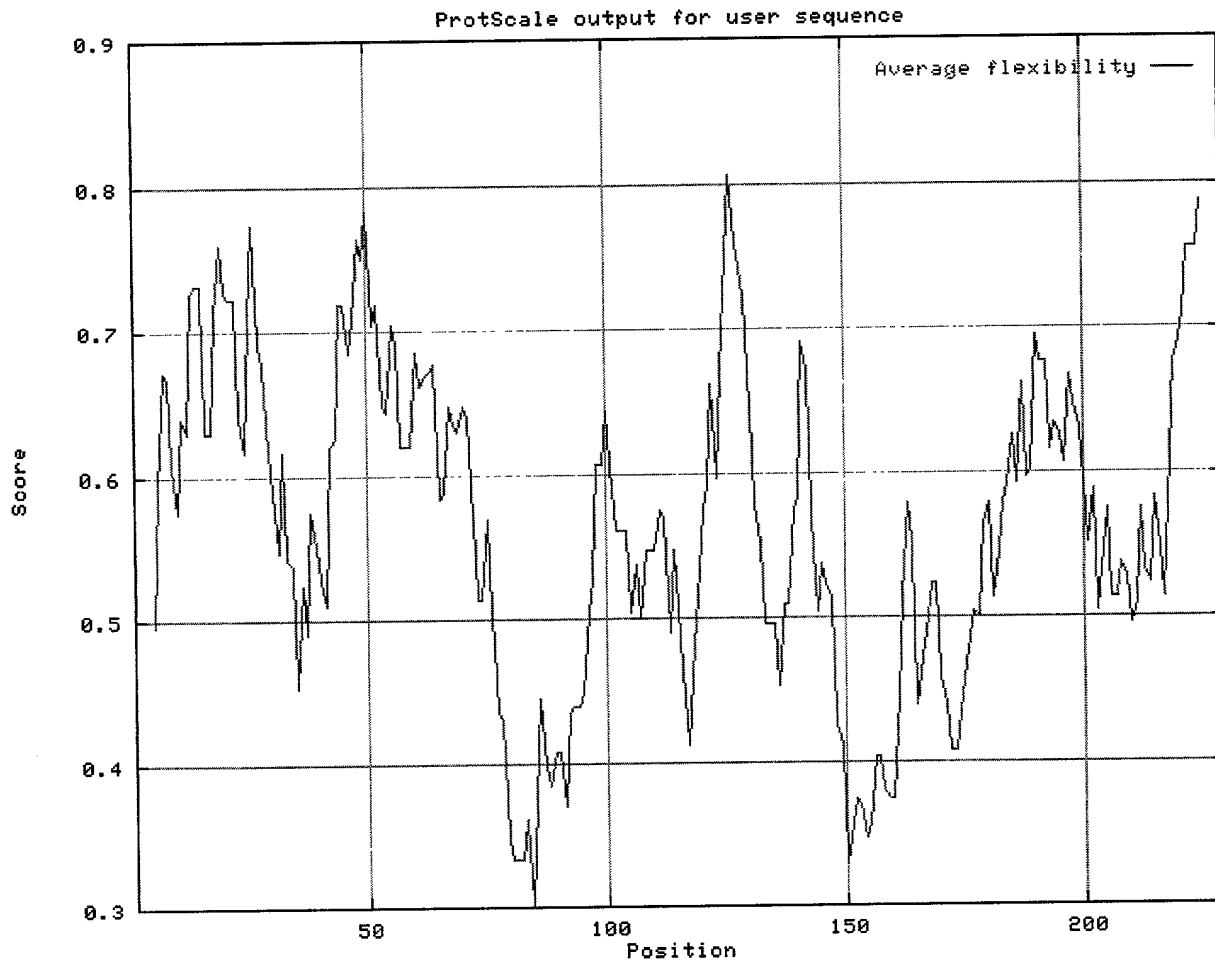


Figure 9: 85P1B3 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

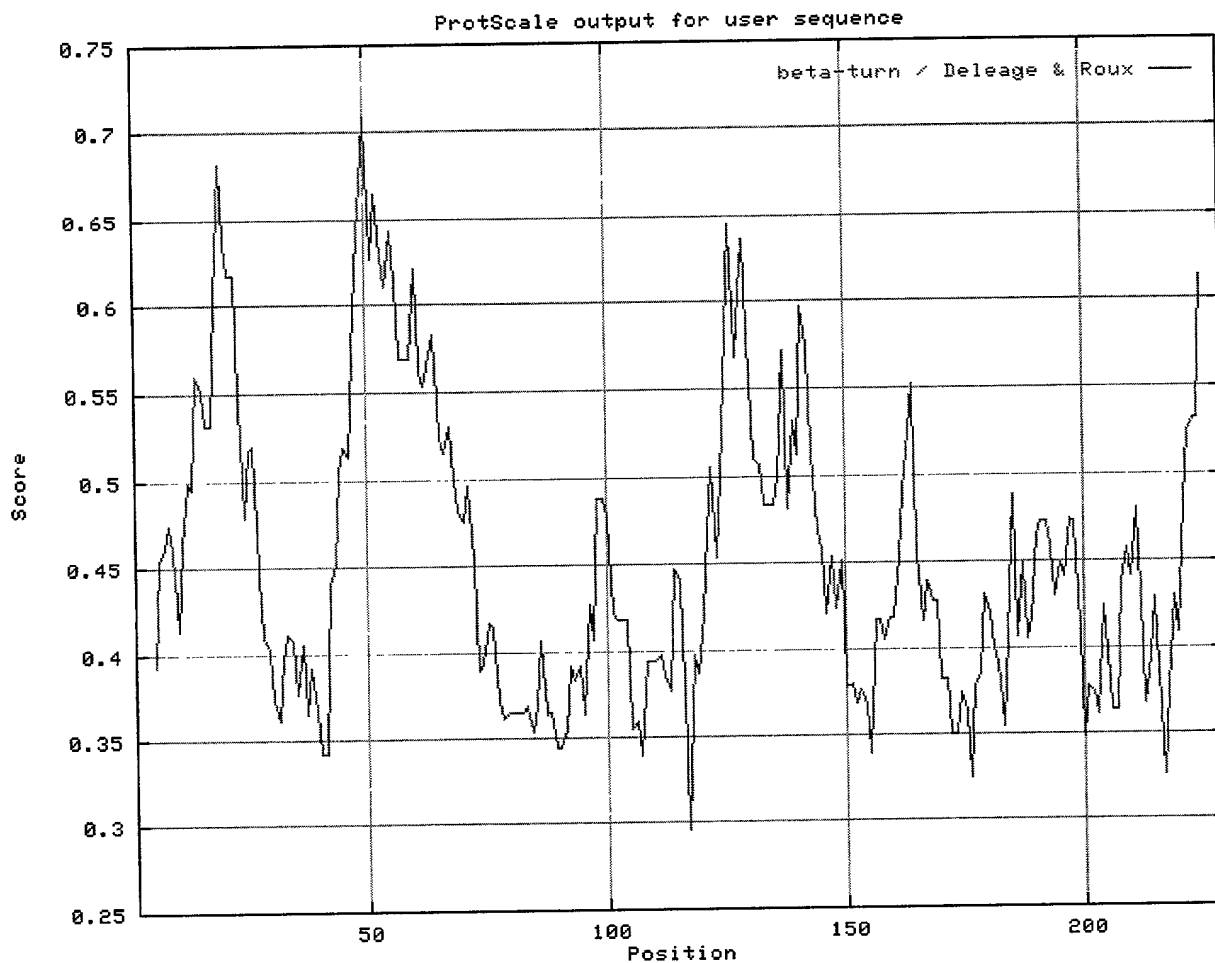


Figure 10 RT-PCR analysis of 85P1B3 expression.

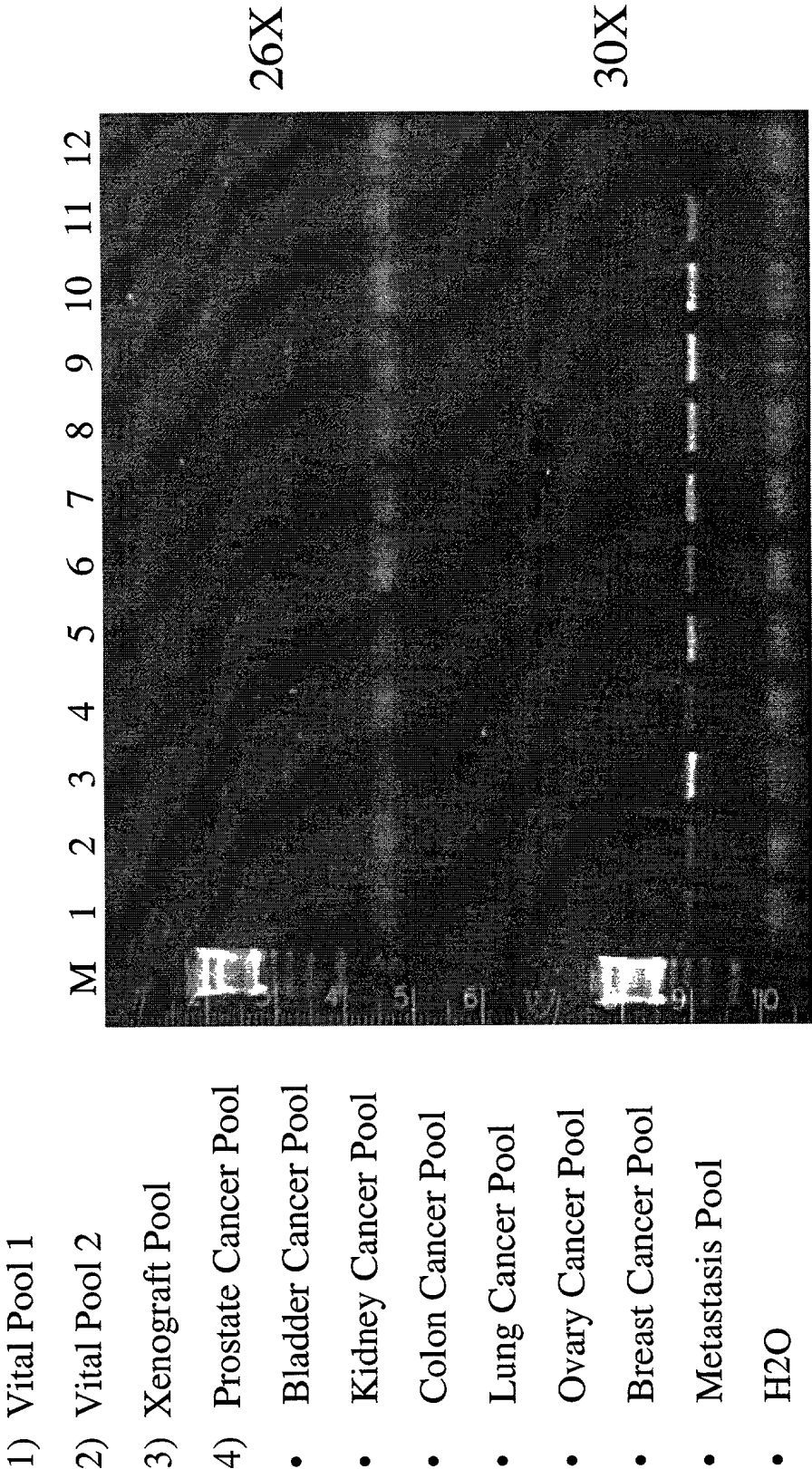


Figure 11 Expression of 85P1B3 in Normal Human Tissues

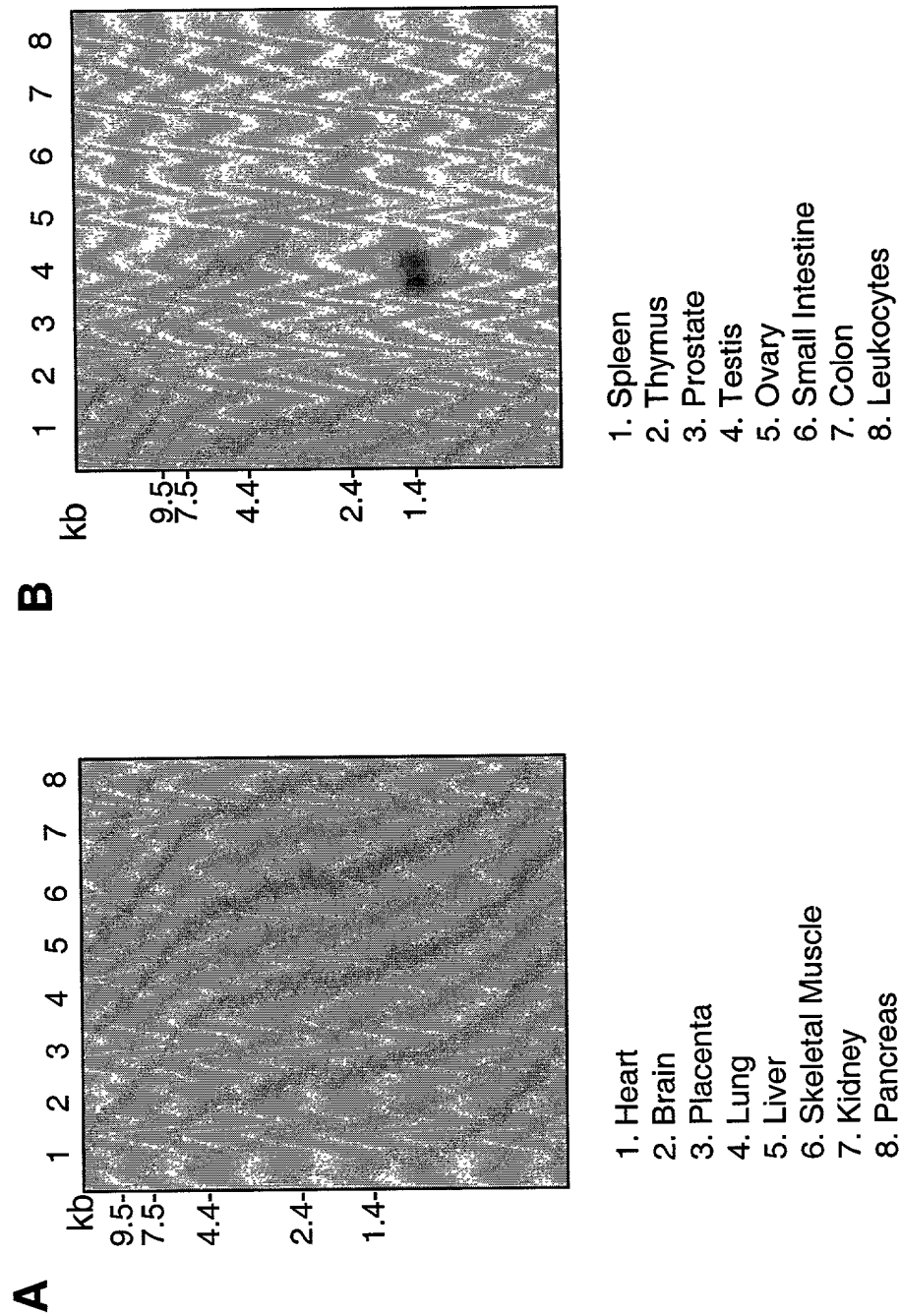


Figure 12 Expression of 85P1B3 in Human Cancer Cell lines

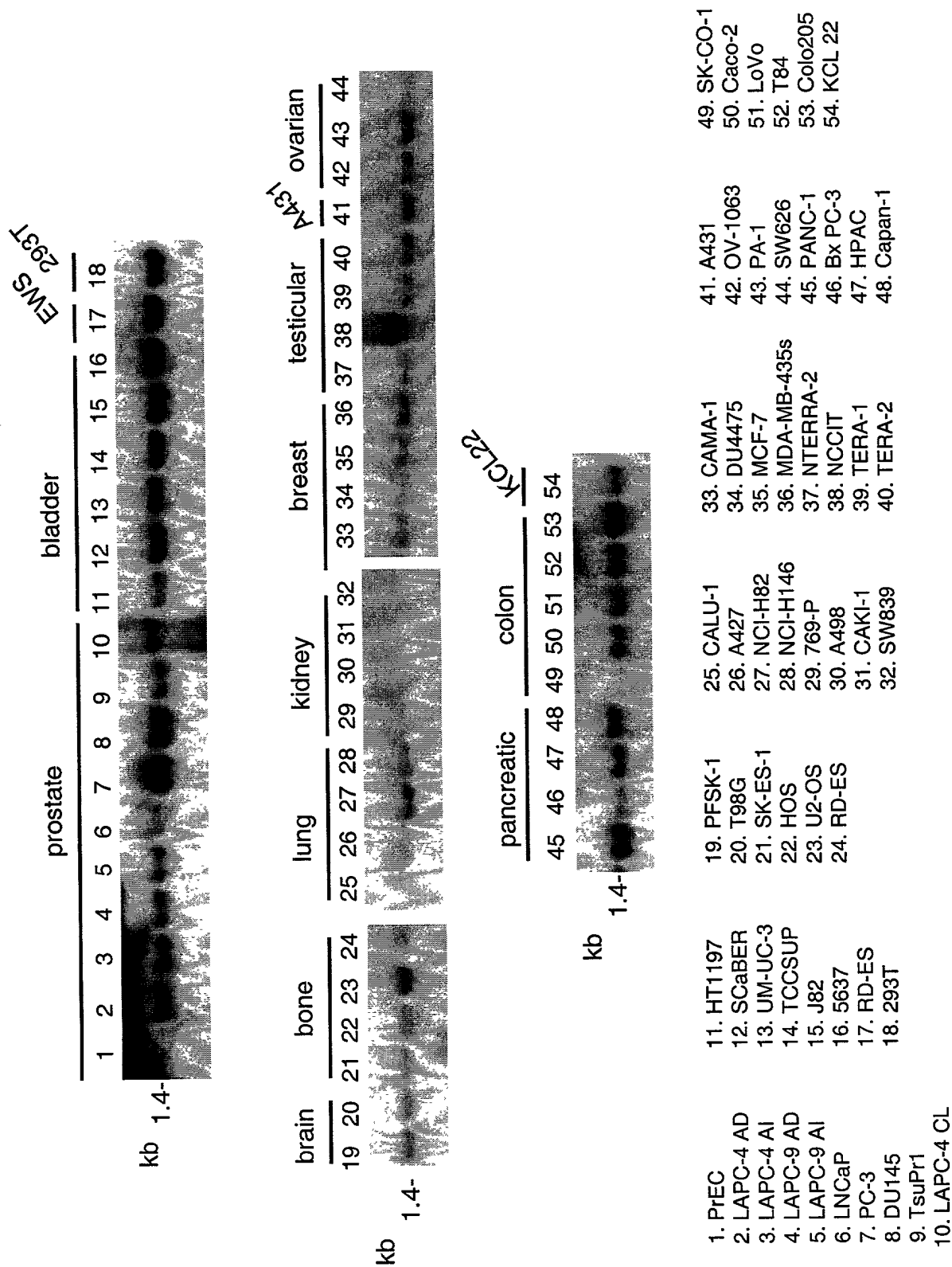


Figure 1: Schematic representation of the experimental design. The figure is divided into two main sections: 'normal' and 'cancer'. The 'normal' section shows three organs: breast, prostate, and cervix. The 'cancer' section shows three organs: stomach, lung, and cancer cell lines. Each organ is represented by a rectangular box containing several black dots, which represent the locations of the organs in the body. The 'normal' section is labeled 'normal' and the 'cancer' section is labeled 'cancer'.

T = tumor RNA

N = normal adjacent tissue RNA

Cancer cell lines are:
(from left to right)

HeLa (cervical carcinoma)

Daudi (Burkitt's lymphoma)

K562 (CML)

HL-60 (PML)

G361 (melanoma)

A549 (lung carcinoma)

MOLT-4 (lymphoblastic leuk.)

SW480 (colorectal carcinoma)

Raji (Burkitt's lymphoma)

P1 – Stage III, T2N1MX
P2 – Stage III, T3N1MX

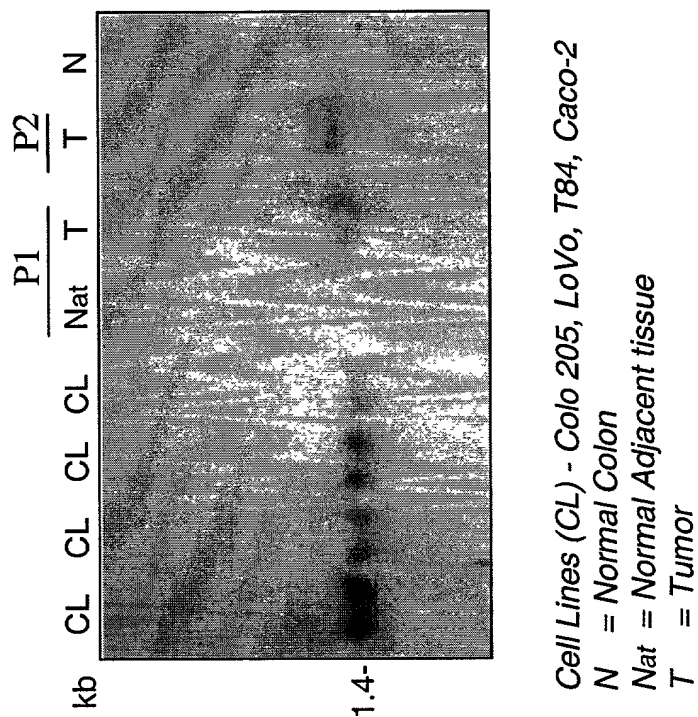


Figure 15 Expression of 85P1B3 in Bladder Cancer Patient Specimens

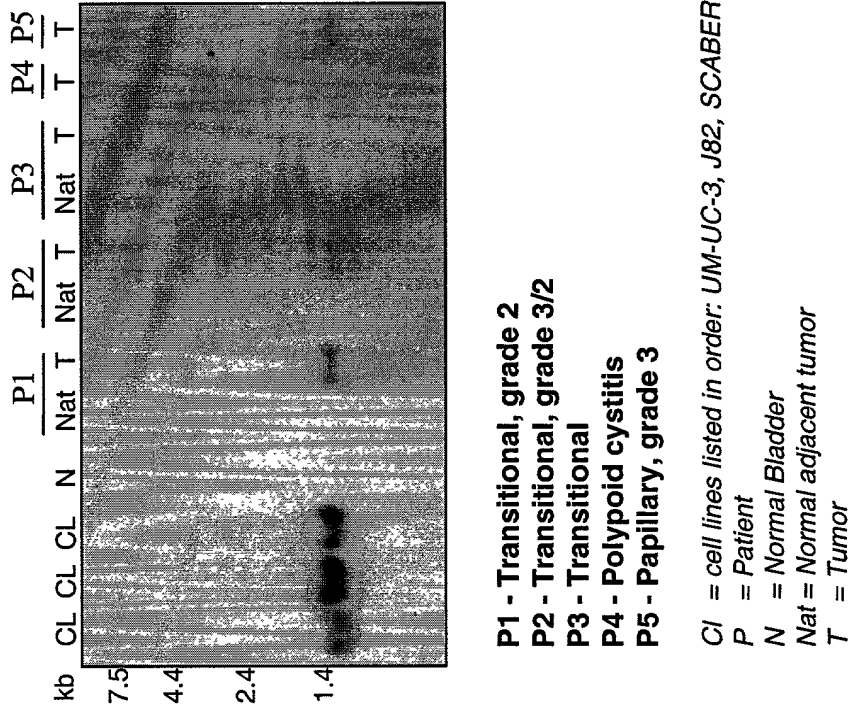


Figure 16 Expression of 85P1B3 in Lung Cancer Patient Specimens

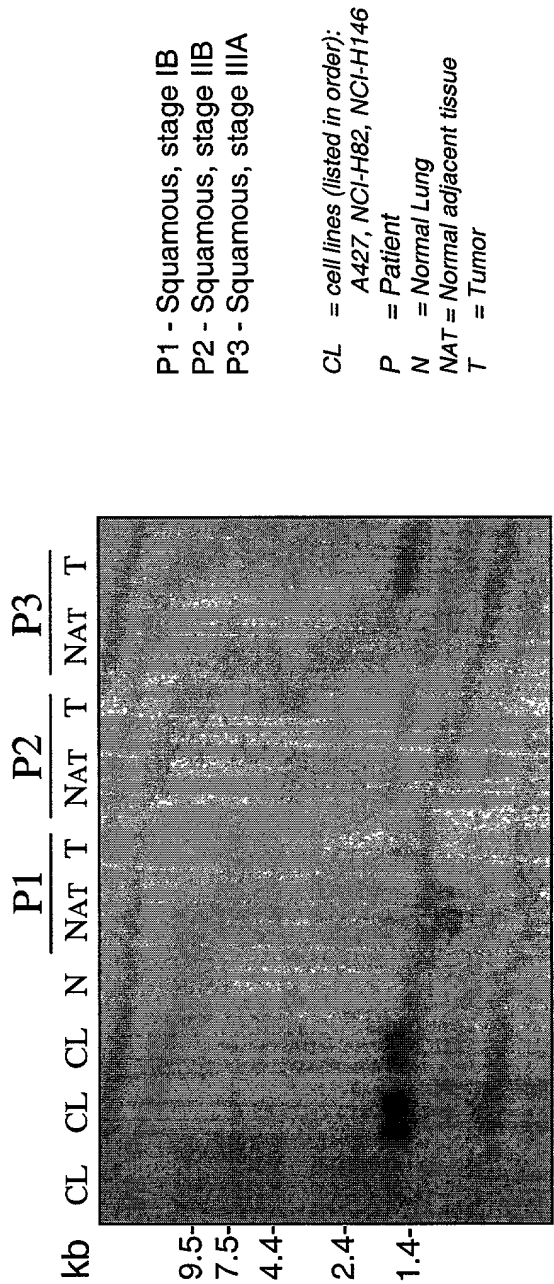


Figure 17 Expression of 85P1B3 in Prostate Cancer Xenografts Following Castration

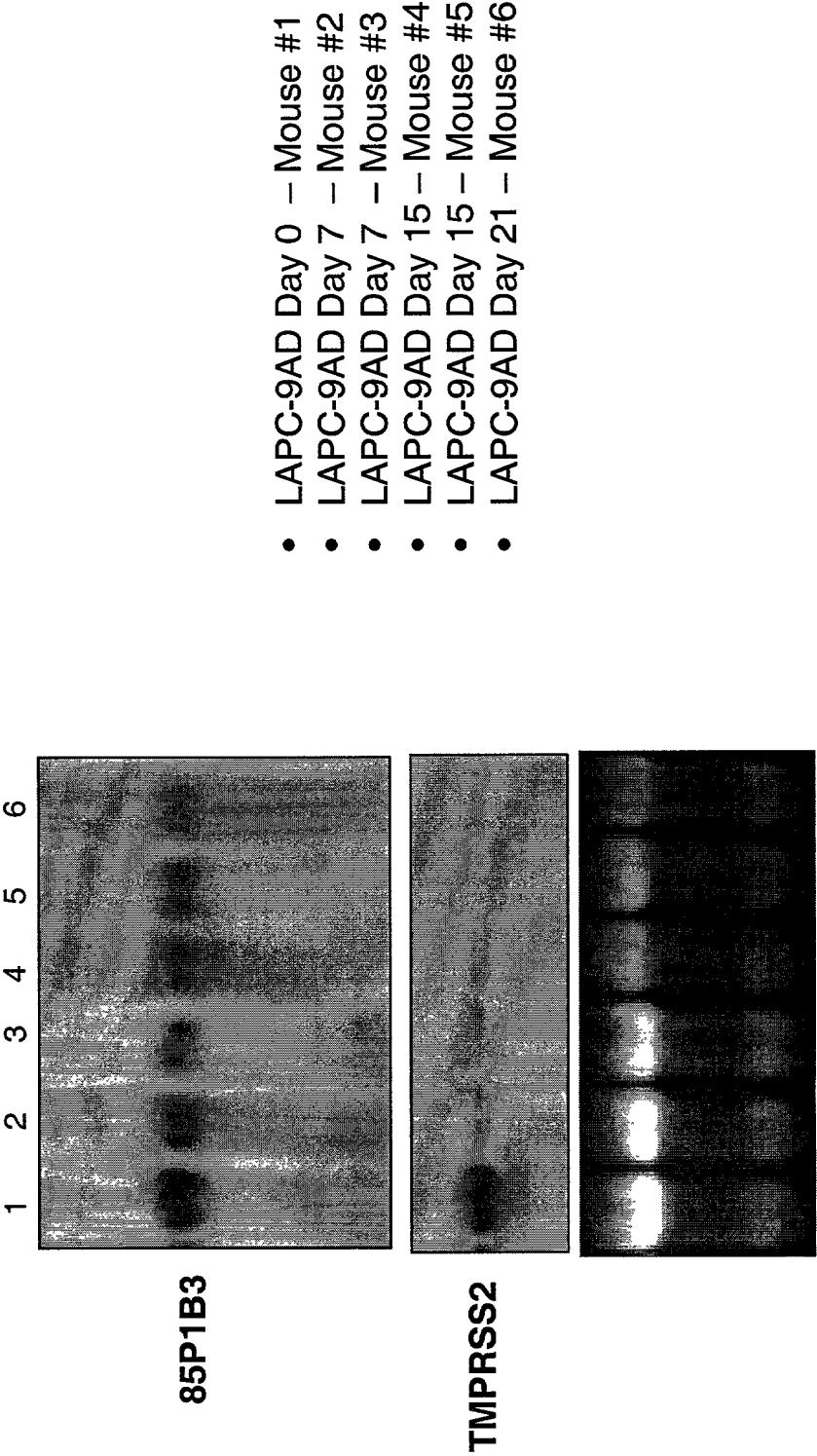


Figure 18 Expression of 85P1B3 in PC3 Cells Following Retroviral-Mediated Gene Delivery

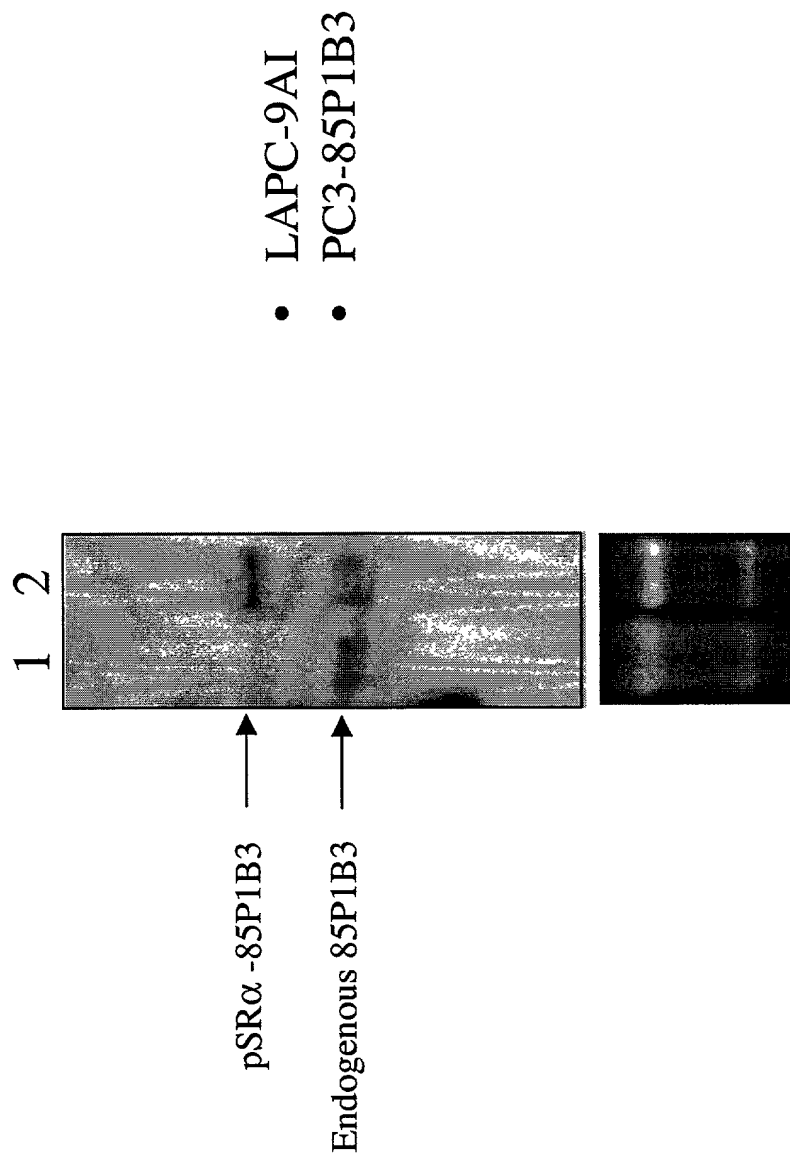
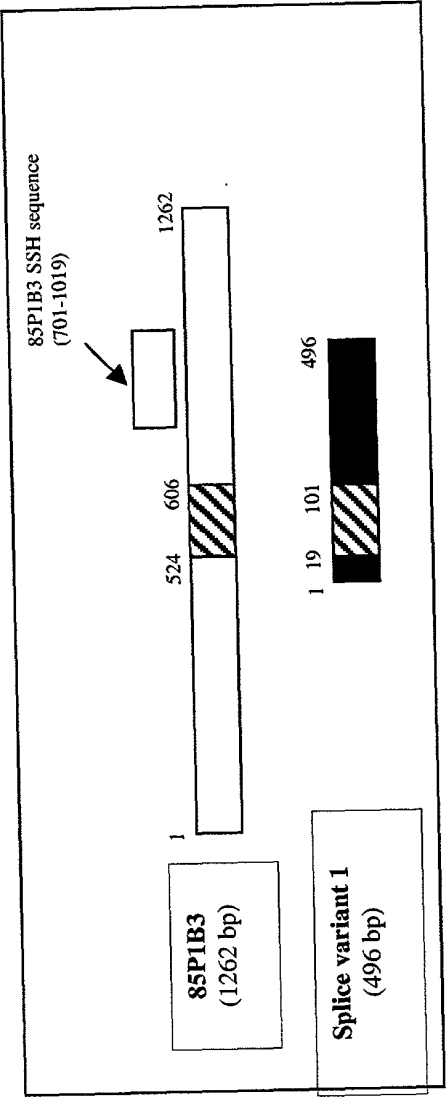


Figure 19.



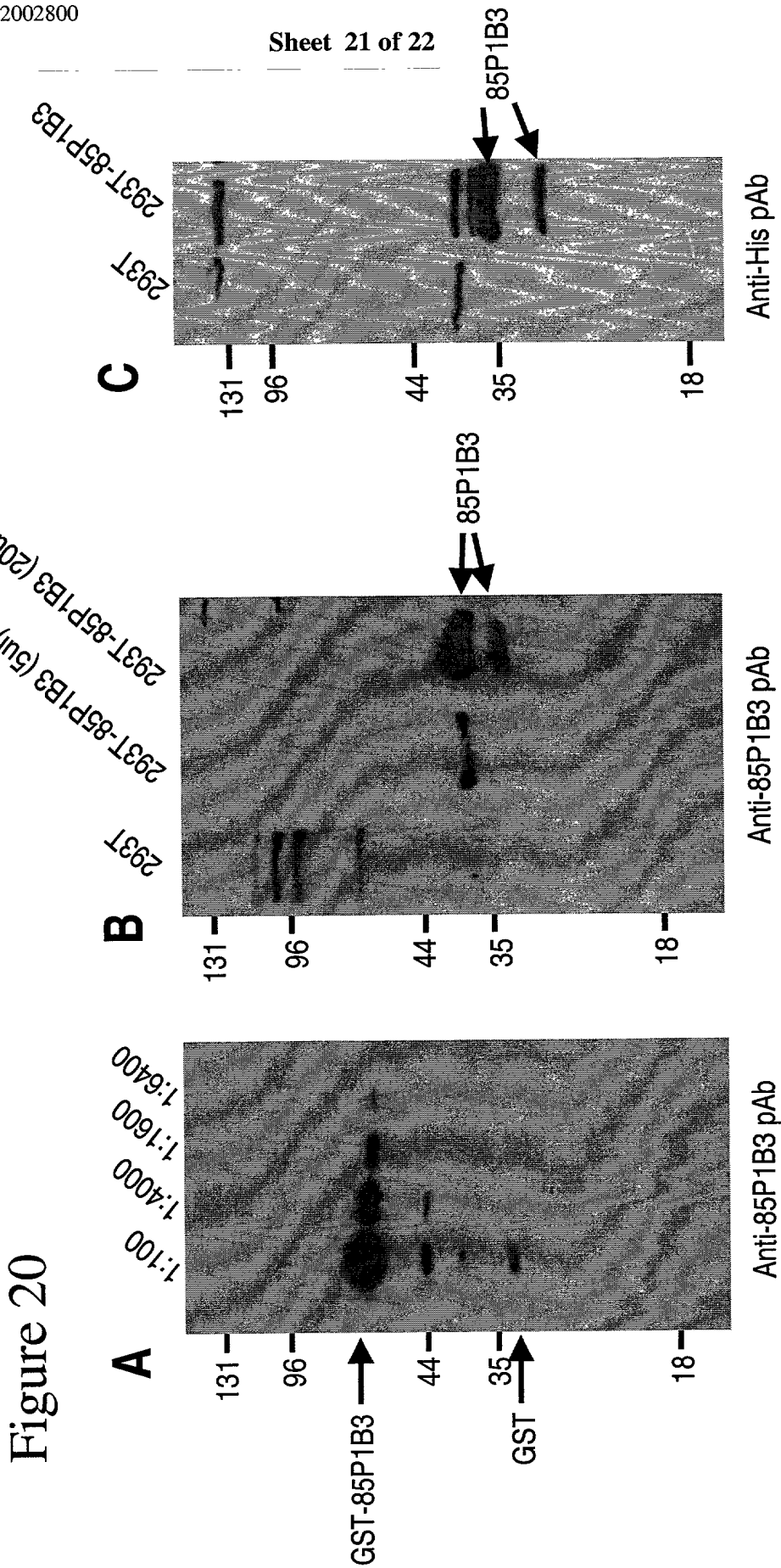


Fig. 21A

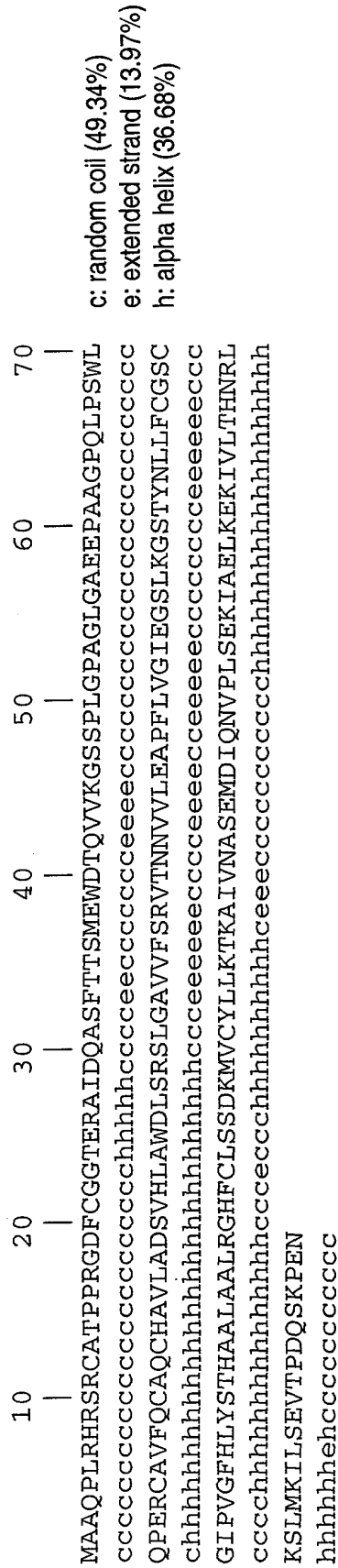


Fig. 21B

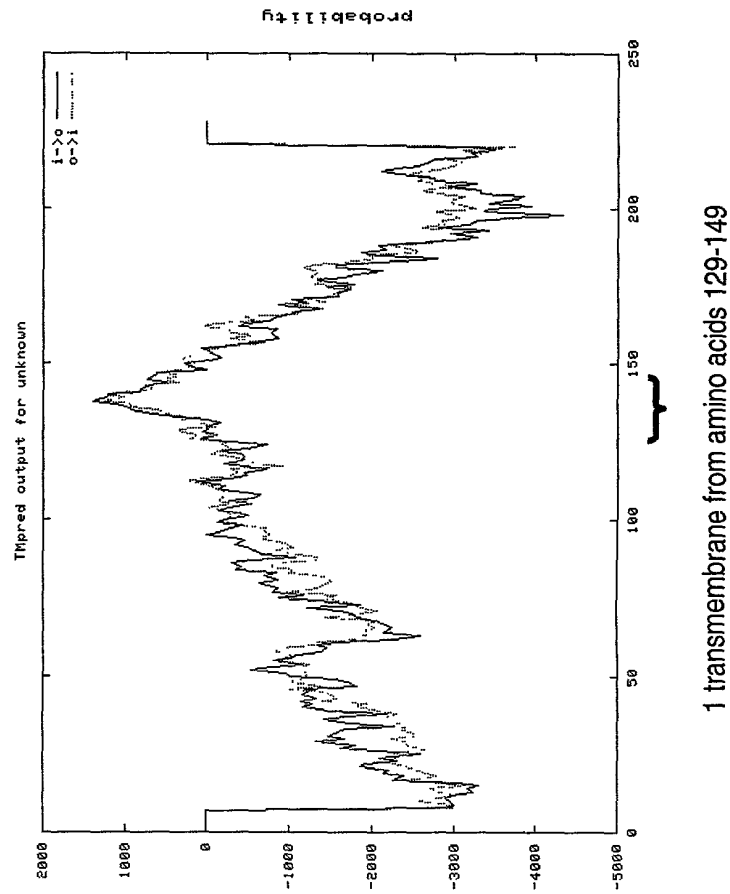


Fig. 21C

